

OIIPE

RAW SEQUENCE LISTING

DATE: 04/30/2001

PATENT APPLICATION: US/09/832,501

TIME: 09:15:46

Input Set : A:\PF542SL.txt

Output Set: N:\CRF3\04302001\I832501.raw

P.S

ENTERED

3 <110> APPLICANT: Ballance, David J.
 4 Sleep, Darrell
 5 Turner, Andrew J.
 6 Sadeghi, Homa
 7 Prior, Christopher P.
 9 <120> TITLE OF INVENTION: Albumin Fusion Proteins
 11 <130> FILE REFERENCE: PF542
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/832,501
 14 <141> CURRENT FILING DATE: 2001-04-12
 16 <150> PRIOR APPLICATION NUMBER: 60/229,358
 17 <151> PRIOR FILING DATE: 2000-04-12
 19 <150> PRIOR APPLICATION NUMBER: 60/256,931
 20 <151> PRIOR FILING DATE: 2000-12-21
 22 <150> PRIOR APPLICATION NUMBER: 60/199,384
 23 <151> PRIOR FILING DATE: 2000-04-25
 25 <160> NUMBER OF SEQ ID NOS: 37
 27 <170> SOFTWARE: PatentIn Ver. 2.1
 29 <210> SEQ ID NO: 1
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 32 <213> ORGANISM: Artificial Sequence
 34 <220> FEATURE:
 35 <221> NAME/KEY: primer_bind
 36 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
 38 <400> SEQUENCE: 1
 39 cccaagaatt cccttatcca ggc 23
 42 <210> SEQ ID NO: 2
 43 <211> LENGTH: 33
 44 <212> TYPE: DNA
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 49 <223> OTHER INFORMATION: primer useful to clone human growth hormone cDNA
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 57 <212> TYPE: DNA
 58 <213> ORGANISM: Artificial Sequence
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 61 <221> NAME/KEY: misc_structure
 62 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
 63 with non-cohesive ends.
 65 <400> SEQUENCE: 3
 66 gataaagatt cccaac 16
 69 <210> SEQ ID NO: 4
 70 <211> LENGTH: 17

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71 <212> TYPE: DNA
72 <213> ORGANISM: Artificial Sequence
74 <220> FEATURE:
75 <221> NAME/KEY: misc_structure
76 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
77     with non-cohesive ends.
79 <400> SEQUENCE: 4
80 aattgttggg aatcttt                                     17
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 17
85 <212> TYPE: DNA
86 <213> ORGANISM: Artificial Sequence
88 <220> FEATURE:
89 <221> NAME/KEY: misc_structure
90 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
91     with non-cohesive ends.
93 <400> SEQUENCE: 5
94 ttagcttat tcccaac                                     17
97 <210> SEQ ID NO: 6
98 <211> LENGTH: 18
99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <221> NAME/KEY: misc_structure
104 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA fragments
105     with non-cohesive ends.
107 <400> SEQUENCE: 6
108 aattgttggg aataagcc                                     18
111 <210> SEQ ID NO: 7
112 <211> LENGTH: 24
113 <212> TYPE: PRT
114 <213> ORGANISM: Artificial Sequence
116 <220> FEATURE:
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118 <222> LOCATION: 1)..(19)
119 <223> OTHER INFORMATION: invertase leader sequence
121 <220> FEATURE:
122 <221> NAME/KEY: SITE
123 <222> LOCATION: 20)..(24)
124 <223> OTHER INFORMATION: first 5 amino acids of mature human serum albumin
126 <400> SEQUENCE: 7
127 Met Leu Leu Gln Ala Phe Leu Phe Leu Ala Gly Phe Ala Ala Lys
128   1           5           10           15
130 Ile Ser Ala Asp Ala His Lys Ser
131           20
134 <210> SEQ ID NO: 8
135 <211> LENGTH: 21
136 <212> TYPE: DNA
137 <213> ORGANISM: Artificial Sequence

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139 <220> FEATURE:
140 <221> NAME/KEY: misc_structure
141 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
142     fragments with non-cohesive ends.
144 <400> SEQUENCE: 8
145 gagatgcaca cctgagtgag g                                21
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149 <211> LENGTH: 27
150 <212> TYPE: DNA
151 <213> ORGANISM: Artificial Sequence
153 <220> FEATURE:
154 <221> NAME/KEY: misc_structure
155 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
156     fragments with non-cohesive ends.
158 <400> SEQUENCE: 9
159 gatactgttg cttcgatgca cacaaga                            27
162 <210> SEQ ID NO: 10
163 <211> LENGTH: 24
164 <212> TYPE: DNA
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168 <221> NAME/KEY: misc_structure
169 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
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173 ctcttggtg catcgaagcc acag                                24
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177 <211> LENGTH: 30
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179 <213> ORGANISM: Artificial Sequence
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182 <221> NAME/KEY: misc_structure
183 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
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186 <400> SEQUENCE: 11
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190 <210> SEQ ID NO: 12
191 <211> LENGTH: 31
192 <212> TYPE: DNA
193 <213> ORGANISM: Artificial Sequence
195 <220> FEATURE:
196 <221> NAME/KEY: misc_structure
197 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
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200 <400> SEQUENCE: 12
201 aattgttggg aataaattct gaggtcttct c                        31
204 <210> SEQ ID NO: 13
205 <211> LENGTH: 47
206 <212> TYPE: DNA

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207 <213> ORGANISM: Artificial Sequence
209 <220> FEATURE:
210 <221> NAME/KEY: misc_structure
211 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
212     fragments with non-cohesive ends.
214 <400> SEQUENCE: 13
215 tttaggcttag gtggcggtgg atccggcggt ggtggatctt tcccaac          47
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219 <211> LENGTH: 48
220 <212> TYPE: DNA
221 <213> ORGANISM: Artificial Sequence
223 <220> FEATURE:
224 <221> NAME/KEY: misc_structure
225 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
226     fragments with non-cohesive ends.
228 <400> SEQUENCE: 14
229 aattgttggg aaagatccac caccgcccga tccaccgcca cctaagcc          48
232 <210> SEQ ID NO: 15
233 <211> LENGTH: 62
234 <212> TYPE: DNA
235 <213> ORGANISM: Artificial Sequence
237 <220> FEATURE:
238 <221> NAME/KEY: misc_structure
239 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
240     fragments with non-cohesive ends.
242 <400> SEQUENCE: 15
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244 ac                                                                 62
247 <210> SEQ ID NO: 16
248 <211> LENGTH: 63
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <221> NAME/KEY: misc_structure
254 <223> OTHER INFORMATION: synthetic oligonucleotide used to join DNA
255     fragments with non-cohesive ends.
257 <400> SEQUENCE: 16
258 aattgttggg aaggatccac cgccaccaga tccgcccga ccagatccac caccgcctaa 60
259 gcc                                                                 63
262 <210> SEQ ID NO: 17
263 <211> LENGTH: 1782
264 <212> TYPE: DNA
265 <213> ORGANISM: Homo sapiens
267 <220> FEATURE:
268 <221> NAME/KEY: CDS
269 <222> LOCATION: (1)..(1755)
272 <400> SEQUENCE: 17
273 gat gca cac aag agt gag gtt gct cat cgg ttt aaa gat ttg gga gaa  48
274 Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu

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275	1		5		10		15	
277	gaa	aat	ttc	aaa	gcc	ttg	gtg	ttg att gcc ttt gct cag tat ctt cag 96
278	Glu	Asn	Phe	Lys	Ala	Leu	Val	Leu Ile Ala Phe Ala Gln Tyr Leu Gln
279				20		25		30
281	cag	tgt	cca	ttt	gaa	gat	cat	gta aaa tta gtg aat gaa gta act gaa 144
282	Gln	Cys	Pro	Phe	Glu	Asp	His	Val Lys Leu Val Asn Glu Val Thr Glu
283			35		40		45	
285	ttt	gca	aaa	aca	tgt	gtt	gct	gat gag tca gct gaa aat tgt gac aaa 192
286	Phe	Ala	Lys	Thr	Cys	Val	Ala	Asp Glu Ser Ala Glu Asn Cys Asp Lys
287		50		55		60		
289	tca	ctt	cat	acc	ctt	ttt	gga	gac aaa tta tgc aca gtt gca act ctt 240
290	Ser	Leu	His	Thr	Leu	Phe	Gly	Asp Lys Leu Cys Thr Val Ala Thr Leu
291	65			70		75		80
293	cgt	gaa	acc	tat	ggt	gaa	atg	gct gac tgc tgt gca aaa caa gaa cct 288
294	Arg	Glu	Thr	Tyr	Gly	Glu	Met	Ala Asp Cys Cys Ala Lys Gln Glu Pro
295			85		90		95	
297	gag	aga	aat	gaa	tgc	ttc	ttg	caa cac aaa gat gac aac cca aac ctc 336
298	Glu	Arg	Asn	Glu	Cys	Phe	Leu	Gln His Lys Asp Asp Asn Pro Asn Leu
299			100		105		110	
301	ccc	cga	ttg	gtg	aga	cca	gag	ggt gat gtg atg tgc act gct ttt cat 384
302	Pro	Arg	Leu	Val	Arg	Pro	Glu	Val Asp Val Met Cys Thr Ala Phe His
303			115		120		125	
305	gac	aat	gaa	gag	aca	ttt	ttg	aaa aaa tac tta tat gaa att gcc aga 432
306	Asp	Asn	Glu	Glu	Thr	Phe	Leu	Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
307		130		135		140		
309	aga	cat	cct	tac	ttt	tat	gcc	cgg gaa ctc ctt ttc ttt gct aaa agg 480
310	Arg	His	Pro	Tyr	Phe	Tyr	Ala	Pro Glu Leu Leu Phe Phe Ala Lys Arg
311	145			150		155		160
313	tat	aaa	gct	gct	ttt	aca	gaa	tgt tgc caa gct gct gat aaa gct gcc 528
314	Tyr	Lys	Ala	Ala	Phe	Thr	Glu	Cys Cys Gln Ala Ala Asp Lys Ala Ala
315			165		170		175	
317	tgc	ctg	ttg	cca	aag	ctc	gat	gaa ctt cgg gat gaa ggg aag gct tcg 576
318	Cys	Leu	Leu	Pro	Lys	Leu	Asp	Glu Leu Arg Asp Glu Gly Lys Ala Ser
319			180		185		190	
321	tct	gcc	aaa	cag	aga	ctc	aaa	tgt gcc agt ctc caa aaa ttt gga gaa 624
322	Ser	Ala	Lys	Gln	Arg	Leu	Lys	Cys Ala Ser Leu Gln Lys Phe Gly Glu
323			195		200		205	
325	aga	gct	ttc	aaa	gca	tgg	gca	gtg gct cgc ctg agc cag aga ttt ccc 672
326	Arg	Ala	Phe	Lys	Ala	Trp	Ala	Val Ala Arg Leu Ser Gln Arg Phe Pro
327		210		215		220		
329	aaa	gct	gag	ttt	gca	gaa	ggt	tcc aag tta gtg aca gat ctt acc aaa 720
330	Lys	Ala	Glu	Phe	Ala	Glu	Val	Ser Lys Leu Val Thr Asp Leu Thr Lys
331	225			230		235		240
333	gtc	cac	acg	gaa	tgc	tgc	cat	gga gat ctg ctt gaa tgt gct gat gac 768
334	Val	His	Thr	Glu	Cys	Cys	His	Gly Asp Leu Leu Glu Cys Ala Asp Asp
335			245		250		255	
337	agg	gcg	gac	ctt	gcc	aag	tat	atc tgt gaa aat cag gat tcg atc tcc 816
338	Arg	Ala	Asp	Leu	Ala	Lys	Tyr	Ile Cys Glu Asn Gln Asp Ser Ile Ser
339			260		265		270	

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

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L:13 M:270 C: Current Application Number differs, Replaced Current Application Number
L:712 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:801 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:890 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:980 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32
L:1287 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33